us-09-403-724-5.rag

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July 17, 2001, 16:55:27 ; Search time 37.5 Seconds
(without alignments)
415.476 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                           OM protein - protein search, using sw model
                                                                                                                                                                   Run on:
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1415 1 CGLRLLHRRQKRIIGGKNSL.....PGVYTKVSAFVPWIKSVTKL 257 US-09-403-724-5 Title: Perfect score: Sequence:

412676 seqs, 60623988 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

412676 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

A_Geneseq_0601:* Database :

/SID88/gcgdata/geneseq/geneseqp/AA1980.DAT:*
/SID88/gcgdata/geneseqg/geneseqp/AA1981.DAT:*
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/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:* DAT: * DAT: * DAT: * /SIDS8/qcqdata/geneseq/geneseqp/AA2000.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1989 /SIDS8/gcgdata/geneseq/geneseqp/AA1990 /SIDS8/gcgdata/geneseq/geneseqp/AA1991 /SIDS8/gcgdata/geneseq/geneseqp/AA1992 /SIDS8/gcgdata/geneseq/geneseqp/AA1993

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Description	Human serine prote Human neurotrypsin Mouse serine prote Mouse neurotrypsin t-PA deletion vari Sequence of coding Human tissue PA va Novel tissue plasm t-PA variant H432A Human t-PA variant	Human t-PA variant
SUMMARIES	44444444	AAR70903
DB	20 20 20 20 11 10 11 11 11	16
Length	822 875 761 761 526 437 483 527 527	
% Query Match Length DB	100.0 100.0 91.7 91.7 33.0 32.8 32.8 32.8	32.8
Score	1415 1415 1298 1298 467 463 5463 463 5463 5463 5	463.5
Result No.	10243078901	11

Sequence of tissue t-PA deletion vari	plasm	Amino acid sequenc	eleti	serine	serine	Human serine prote	insertion va	e Serine	t-PA deletion vari	t-PA deletion vari	t-PA variant R449A	Human t-PA variant	Human t-PA variant	nt hav	Sequence of full l	T-PA variant havin	3 t-PA V	t-PA deletion vari	deletion	tissue	tissue	Human tissue PA va		tis		_	tissue	sne	ane	sane	Human tissue PA va	Human tissue PA va
AAR04700 AAR09230	AAP82582	AAW46917	AAR09228	AAY44426	AAY72108	AAY72092	AAR09216	AAY44427	AAR09229	AAR09238	AAR09281	AAR70871	AAR70906	AAR13154	AAP30001	AAR12423	AAR13442	AAR09225	AAR09226	AAR70889	AAR79144	AAR70884	AAR70885	AAR70886	AAR70887	AAR70888	AAR70850	AAR70852	AAR70851	AAR70853	AAR70854	AAR70855
	6		11	21	21	21	11	71	1	11	11	16				a	2	11	11	16	16	16	16	16	16	16	16	16	16	16	16	16
562 525	562	356	526	1042	296	372	528	1113	526	525	527	527	527	559	562	562	562	526	526	483	483	483	483	483	483	483	483	483	483	483	483	483
32.8	~	~	· ~	ς.	ς.	ď	ď	ď.	ď	~;	ď.	ζ.	α.	7	2	2	ď	α.	ζ.	$^{\circ}$	$^{\circ}$	$^{\circ}$	32.4	$^{\circ}$	$^{\circ}$	C	ď.	~	2	α.		$^{\circ}$
463.5	62	4	462	462	461	461	461	461	460	σ	53	459.5	5	5	5	5	5	4	459		55		5						5			
12	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Yamaguchi N, Yamashiro K;
                                                      Serine protease; BSSP-3; brain tissue.
     AAW99087 standard; Protein; 822 AA.
                                          Human serine protease BSSP-3.
                                                                                                      98WO-JP03324
                                                                                                                  97JP-0213969.
                              (first entry)
                                                                                                                               (SUNR ) SUNTORY LTD.
                                                                                                                   24 - JUL-1997;
                                                                   Homo sapiens
                                                                              WO9905290-A1
                                                                                                      24-JUL-1998;
                              13-MAY-1999
                                                                                                                                           Tsuruoka N,
                                                                                           04-FEB-1999.
                 AAW99087;
AAW99087
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New serine protease expressed in brain tissue - used in screening for potential serine protease inhibitors for drug use

WPI; 1999-142942/12. N-PSDB; AAX19024. Claim 1; Page 61-65; 69pp; Japanese.

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0;
                                                                           The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                            685 kglftgrmlcagnlqednrvdscqgdsggplmcekpdeswvygvtswgygcgvkdtpgv 744
                                                                                                                                                                                                                                                                                                                       61 KRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQ 120
                                                                                                                                                                                                                                                                                                                                    Mouse; neurotrypsin; tumour inhibition; neurological disease; lung disease; gene therapy; drug development; stroke; brain injury; neurodegeneration; neuroinflammatory disease; multiple sclerosis; epilepsy; hypoxia; ischaemia; nerve transection; neoangiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                    KGRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGV
                                                                                                                                                                                                                                                              1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCF

    used in screening

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0
                                                                                                                                                                                                       Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   New serine protease expressed in brain tissue - used ifor potential serine protease inhibitors for drug use
                                                                                                                                                                                                         91.7%; Score 1298; DB 20; 90.3%; Pred. No. 7.4e-108;
                                                                                                                                                                                                                                     12; Mismatches
                                                   Example 1; Page 51-54; 69pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW83362 standard; Protein; 761 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97CH-0000966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-IB00625
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745 ytrvpafvpwiksvtsl 761
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                                                                                                                                                                                                                                     Matches 232; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 emphysema; bronchitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-009438/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse neurotrypsin.
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                 761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAV72590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sonderegger P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW83362;
                                                                                                                                                                  Sequence
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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The present sequence represents mouse neurotrypsin. Neurotrypsin proteins and polynucleotides can be used: (i) to inhibit tumours, including caused polynucleotides can be used: (i) to inhibit tumours, including caused by stroke or brain injury (having a protective effect on the caused by stroke or brain injury (having a protective effect on the convenience) of increases errors of amanged neurons (e.g. multiple sclerosis) or epilepsy; (iv) to increase survival of damaged neurons (e.g. in cases of hypoxia, ischaemia, nerve transection) and to stimulate regeneration and/or restoration of synapses; (v) to treat or prevent retinal disorders (e.g. degeneration or neoanglogenessis); (vi) to prevent apoptosis (or other causes of cell death) in the nervous system; (vii) to regenerate brain and/or nervous tissue; (viii) to treat pain; (ix) to improve brain or wide range of psychiatric disorders; and (xi) to treat or prevent a prevent a wide range of psychiatric disorders; and (xi) to treat or prevent a injury associated with protease expression (specifically emphysema or bronchitis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 KGRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMCERPGESWVVYGVTSWGYGCGVKDSPGV 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CARFSSHVLPACLPLWRERPQKTASNCYITGWGDTGRAYSRTLQQAAIPLLPKRECEERY
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/label= deletion

/note= "the amino acid at position 303 of the

/note= "type mature t-PA has been deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
human and murine neurotrypsin - used, e.g. for inhibiting ours, treatment of neurological or lung disease, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.7%; Score 1298; DB 20; Length 761; 90.3%; Pred. No. 7.4e-108; Live 12; Mismatches 13; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue plasminogen activator; zymogen; clot; plasma; plasmin.
                                   gene therapy and in drug development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR09227 standard; protein; 526 AA.
                                                                     Claim 1; Page 29-32; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t-PA deletion variant d303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 YTKVSAFVPWIKSVTKL 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 91.75
Best Local Similarity 90.33
Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-FEB-1993
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                          cumours,
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169 PLLPKRFCEERY--KGRFTGRMLCAG-----NLHEHKRVDSCQGDSGGPLMCERPG 217

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This sequence is one of a series of fibrinolytically active variant t-PAs (see AAR70843-70908 + AAR79144). The variants are modified to contain one or more amino acid substitutions, which provide a Asn. *Ser. Thr. tripeptidyl sequence starting at the positions 57-61, 63-69, 99, 101, 103-105, 106, 107, 109, 112, or 250 of the wild type tropamino acid sequence. The Asn of the tripeptidyl sequence contains an N-linked glycosylation site. The variant t-PAs exhibit fibrinolytic activity and have longer half-lives and slower clearance rates from the blood as compared to native t-Pa. The variants can be used as clot-dissolving agents in the treatment of vascular diseases or conditions such as deep vein thrombosis or peripheral arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (t-PA) variant deltal-44,N103,K210,E275,1277.

This sequence varies from the wild type sequence (AAR70842) by:
(a) a deletion of anino acids (AA) 1.44,
(b) substitution of AA at pos.: 103 - G to N; 210 - I to K; 275 - R to E; 277 - K to I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The numbers correspond to the residue positions in the wild type t-PA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amino acid sequence of the human tissue plasminogen activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New tissue plasminogen activator variants - having an N-linked tri:peptidyl glycosylation sequence inserted to increase plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32.8%; Score 463.5; DB 16; Length 483; 38.9%; Pred. No. 1.6e-33;
                                                                                                                                                                                                       label- N-linked glycosylation site
                                                                                                                                                                                                                                     label= N-linked glycosylation site
                                                                                                                                                                                                                                                                 /label= N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keyt BA, Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                       88US-0196909.
                                                                                                                                                                                                                                                                                                                                                                                                  90US-0480691.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; ; 34pp; English.
                                                                                                                                                            397..413
                                                                                                                                271..340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-081536/11.
Disulfide-bond
            Disulfide-bond
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Disulfide-bond
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Disulfide-bond
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                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                          20-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                        20-MAY-1988;
                                                                                                                                                                                                                                                                                               US5385732-A
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-MAR-1993
                                                                                                                                                                                                                                                                                                                            31-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1992
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60 F-KRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tPA with N-terminal peptide of plasminogen linked is more stable in vivo than the native form. It is useful as a thrombolytic agent in the treatment of vascular diseases eg myocardial infarction,
                                                                                                                                                                     Novel tissue plasminogen activator (tPA) encoding plasmid pTPA102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New tissue plasminogen activator - having N-terminal peptide of plasminogen linked to tissue plasminogen activator for increased stability in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 527;
                                                                                                                                                                                                Fibrin; clotting; thrombolytic; vascular disease; stroke; myocardial infarction; heart attack; pulmonary embolism; ds;
                                                                                                                                                                                                                                                                                                                                                                                                      Kusunoki C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,8%; Score 463.5; DB 1 38.9%; Pred. No. 1.8e-33;
218 ESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 252
               :| |: ||| || || ||||||||| :: ||:
445 rmtlv-giiswglgcggkdvpgvytkvtnyldwir 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Otsuka K,
                                                                                            AAR06236 standard; protein; 527 AA
                                                                                                                                                                                                                                                                                                                                                                                                      Satoh S, Suzuki S,
                                                                                                                                                                                                                                                                                                                          90EP-0100457
                                                                                                                                                                                                                                                                                                                                                  89GB-0001422
                                                                                                                                                                                                                                                                                                                                                                             (FUJI ) FUJISAWA PHARM KK.
                                                                                                                                                  11-DEC-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pulmonary embolism etc.
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Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          527 AA;
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                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                          10-JAN-1990;
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                                                                                                                        AAR06236;
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                                                                                 AAR06236
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10;

10;

39; Gaps

88; Indels

41; Mismatches

Matches 107; Conservative

Query Match Best Local Similarity

220 cglrqysqpqfriigglfadiashpwqaaifakhrrspgerflcggillsscwilsaahc 279

qq

ò

1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHC 59

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05-OCT-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-1990;
21-JAN-1992;
22-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-MAY-1988;
                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5385732-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-MAY-1988
                                                                                                                                                                                                                                                                                                Disulfide-
                                                                                                                                                                                                                                                                                                                Disulfide-
Disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disulfide-
                                                                                                                                                                                                                                                                                                                                                                    Disulfide-
                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                         Domain
                                                                                                                                                                                     Domain
                                                                                                                                                                                                                Domain
                                                                                                                                             Key
  The amino acid sequence of the human tissue plasminogen activator (t-PA) variant N67,4432,4434.

This sequence varies from the wild type sequence (AAR70842) by This sequence sorrespond to the residue positions in the wild type t-PA. The numbers correspond to the residue positions in the wild type t-PA. This sequence is one of a series of fibrinolytically active variant three sequence is one of a series of fibrinolytically active variant. This sequence is one of a ARR70843. The variants are modified to contain one or more amino acid substitutions, which provide an ASE/Thr tripeptidyl sequence starting at the positions 57-61, 63-69, 99, 101, 103-105, 106, 107, 109, 112, or 250 of the wild type t-PA amino acid sequence. The Asn of the tripeptidyl sequence contains an N-linked glycosylation site. The variant t-PAs exhibit fibrinolytic activity and have longer half-lives and slower clearance rates from the cold:solving agents in the treatment of vascular diseases or conditions such as deep vein thrombosis or peripheral arterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 EQCARFSSHVLPACLPL-----WRERPQKTASNCYITGWGD---TGRAYSRTLQQAAI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 PLLPKRFCEERY -- KGRFTGRMLCAG-----NLHEHKRVDSCQGDSGGPLMCERPG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434 alypssrctsqhllnhtvtdnmlcagdtrsggpqanlh----dacqgdsggplvclndg 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F-KRYGNSTRSYAVRVGDYHTLVPEEFEEIGVQQIVIHREYRPDRSDYDIALVRLQGPE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.8%; Score 463.5; DB 16; Length 527;
38.9%; Pred. No. 1.8e-33;
tive 41; Mismatches 88; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHC 59
                                                                                                                                                                                                              New tissue plasminogen activator variants - having an N-linked tri:peptidyl glycosylation sequence inserted to increase plasma half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 ESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| |: ||| || || ||||||||: :: ||:
489 rmtlv-giiswglgcggkdvpgvytkvtnyldwir 522
                                                                                                                                                             Presta LG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR70903 standard; Protein; 527 AA
                                                                                                                                                                Keyt BA,
                                                                           90US-0480691.
92US-0824740.
93US-0035427.
                                   88US-0196909
                                                               88US-0196909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 38.9%
Matches 107; Conservative
                                                                                                                                                                                                                                                                             Claim 12; ; 34pp; English.
                                                                                                                                                                Anderson S, Brady KM,
                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                      WPI; 1995-081536/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   527 AA;
                                   20-MAY-1988;
                                                                              15-FEB-1990;
21-JAN-1992;
                                                                                                        22-MAR-1993;
                                                               20-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thrombosis.
        31-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR70903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR70903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 axax
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The amino acid sequence of the human tissue plasminogen activator (t-PA) variant N103,A432,A434. This sequence (AAR70842) by substitutions of AA at pos.: 103 - G to N; 432 - H to A; 434 - R to A. The numbers correspond to the residue positions in the wild type t-PA.
                                       Human wild type tissue plasminogen activator; fibrinolytic; variant; tripeptide; glycosylation site; half-life; clearance rate; blood; clot-dissolving agent; vascular disease; thrombosis; artery; veln.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New tissue plasminogen activator variants - having an N-linked tri:peptidyl glycosylation sequence inserted to increase plasma half-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= N-linked glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tabel serine protease domain
                                                                                                                                                                                                                                                                                               45..91
/label= growth factor domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Presta LG;
                                                                                                                                                                                                                                                                                                                                                  92..173 /
/label= kringle 1 domain
                                                                                                                                                                                                                                                                                                                                                                                                  180..261
/label= kringle 2 domain
                                                                                                                                                                                                                                                                   /label= finger domain
45..91
Human t-PA variant (N103,A432,A434).
                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Keyt BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0196909.
90US-0480691.
92US-0824740.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson S, Brady KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-081536/11.
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(EISA ) EISA KK.
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                                                                                                                                                                             Sequence
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified tissue plasminogen activator; tPA; thrombosis; N-glycosylation.
                                                                                                                                                                           The t-PA variants represented in AAR09215-63 (and the T252R or N184S analogues thereof or combinations thereof) and AAR09266-83 have their fibitinolytic activity turned off when generally in the plasma and activated when proximate to plasmin at the site of the clot thus providing specific localised clot therapy.
                                                                                                                                                                                                                                                                                                                                                            381 rcaqessvvrtvclppadlqlpdwte-----celsgygkhealspfyserlkeahvr 432
                                                                                                                                                                                                                                                                                                                                                  61 -KRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEE 119
                                                                                                                                                                                                                                                                                                                                                                                        120 QCARFSSHVLPACLPL-----WRERPQKTASNCYITGWGD---TGRAYSRTLQQAAIP 169
                                                                                                                                                                                                                                                                                                                                                                                                                              170 LLPKRFCEERY - KGRFTGRMLCAG - - - - - NLHEHKRVDSCQGDSGGPLMCERPGE 218
                                                                                                                                                                                                                                                                                                                                                                                                                                       264 cglrqysqpqfrikgglfadiashpwqaaifakrspge-rflcggilisscwilsaahcf 322
                                                                                                                                                                                                                                                                                         39; Gaps
                                                                                                                                                                                                                                                                                                            1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDGRLLCGATLLSSCWVLTAAHCF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue plasminogen activator with S-119 substd for M and QGI96-98 substd for NGT.
                                                                                                                                                                                                                                                                     DB 11; Length 525;
                                                                              Paoni NF;
                                                                                                                              Modified tissue plasminogen activator – activated only whe proximate to plasmin at site of clot and not systemically
                                                                                                                                                                                                                                                                                          Indels
                                                                              Botstein D, Higgins DL,
                                                                                                                                                                                                                                                                    s; Score 462.5; DB 11;
s; Pred. No. 2.2e-33;
42; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 SWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 252
                                                                                                                                                            Claim 17; Page 43; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP82582 standard; protein; 562
                                                                                                                                                                                                                                                                     32.7%;
39.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87JP-0264339
                              89US-0384608.
88US-0240856.
            89WO-0909997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-NOV-1990 (first entry)
                                                                                                                                                                                                                                                                                         Matches 107; Conservative
                                                                               Anderson S, Bennett WE,
                                                             (GETH ) GENENTECH INC
                                                                                                            WPI; 1990-115987/15.
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                           525 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP63230083-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-1987;
           29-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1988
                               24-JUL-1989;
02-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP82582;
                                                                                         Zoller M;
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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10;
                                                                   Modified tissue plasminogen activator - having glycine-183 and serine-186 residues sustd. With serine and threonine.
                                                                                                                                                                                       One N-glycosylation site, i.e. NSS (117-119) is substituted with NSM and the N-glycosylation is removed. Site 96-98 QGI is changed to NGT. Plasmid encoding the modified tPA is 99-6400 and its transformant is E.coli RR1-Zem 99-6400 (FERM P-9128). This modified tPA, used to treat thrombosis, is of high quality and has a longer half life period in blood. See also AAN82177-N82179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 F-KRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119 EQCARFSSHVLPACLPL-----WRERPQKTASNCYITGWGD---TGRAYSRTLQQAAI 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             417 srcaqessvvrtvclppadlqlpdwre----celsgygkhealspfyserikeahv 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 PLLPKRFCEERY--KGRFTGRMLCAG-----NLHEHKRVDSCQGDSGGPLMCERPG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kallikrein; HKLP; human; serine protease; drug screening; atagonist; agonist; treatment; hypertension; cardiac hypertrophy; arthritis; inflammatory disorder; blood clotting disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSSHGDG-RLLCGATLLSSCWVLTAAHC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.7%; Score 462.5; DB 9; Length 562; 38.9%; Pred. No. 2.4e-33; ative 41; Mismatches 88; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a novel human kallikrein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 ESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIK 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "encoded by YGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "encoded by CRC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW46917 standard; Peptide; 356 AA
                                                                                                                                                         Disclosure; ; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US12724
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WPI; 1988-311961/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                          N-PSDB; N825179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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July 17, 2001, 16:52:11; Search time 37.5 Seconds (without alignments) 1414.560 Million cell updates/sec
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1. /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

2. /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*

3. /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*

4. /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

5. /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*

6. /SIDS8/gcgdata/geneseq-geneseqp/AA1984.DAT:*

7. /SIDS8/gcgdata/geneseq-geneseqp/AA1985.DAT:*

8. /SIDS8/gcgdata/geneseq-geneseqp/AA1985.DAT:*

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9. /SIDS8/gcgdata/geneseq-geneseqp/AA1988.DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                      Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgp/AA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseq/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpaneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpaneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpaneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpaneseqgpAA1999.DAT:*/SIDS8/gcgdata/geneseqgpaneseqg /SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:* /gcgdata/geneseq/geneseqp/AA2000.DAT:*

SUMMARIES

	Description	Human neurotrypsin	Human serine prote	Mouse serine prote	Mouse neurotrypsin	Human SRCR protein	Bovine WC1 protein	Human TANGO 234 ma	Human TANGO 234.	Human TANGO 234 ex	Rat von Ebner's gl	Polypeptide isolat
	ID		AAW99087	AAW99088	AAW83362	AAW64591	AAB66088	AAB66039	AAB66037	AAB66040	AAW07609	AAB19127
	DB	20	20	20	20	19	22	22	22	22	18	21
	Length	875	822	761	761	1785	1436	1413	1453	1319	1290	757
% Ouery	Match Length DB	100.0	94.1	71.0	71.0	20.1	16.9	16.8	16.8	16.7	14.1	13.2
	Score	4905	4617	3481	3481	983.5	830	822.5	822.5	820.5	690.5	645.5
Result	No.	-	7	m	4	ı	9	7	- α	ď	10	11

Human plasminogen SEQ ID 77 of W0991	AAYO8685 AAYO2114 AAYO2114	20	810 810	10.6	517.5 517.5 517.5	4 4 4 5 4 5
	AAY99589	21	791	10.6	517.5	4 n
Plasminogen mutein Human plasminogen,	AAR12944 AAB01887	12	811	10.6	518	39
Plasminogen mutein	AAR12943	12	811	10.6	518	38
plasminogen mutein	AAR12939	12	811	10.6	218	30
Plasminogen mutein	AAR12933	12	811	10.0	518.5	3.5
Plasminogen protei	AAW31169	18	810	10.6	519.5	34
Sequence encoded b	AAR34428	14	810	10.6	520.5	1 m
Human 'Glu' plasmi	AAR12934 AAR60519	122	812	10.6	521.5	H (
Tissue plasminogen	AAP90179	1.0	794	10.7	522.5	30
Plasminogen mutein	AAR12948	17	812	10.7	523.5	8 6 6
Human plasminoden.	AA144420	17	104.2	10.8	528.5	27
Tissue plasminogen	AAP90176	10	704	11.0	538.5	26
Mouse Serine prote	AAY44427	21	1113	11:1	545	25
PA mutant Plg 1-54	AAR20013		1039 807	11.4	559	23
Hybrid plasminogen	AAP80691		1087	11.5	564.5	22
Human SRCR protein	AAW64590		999	11.7	574	21
Human secreted pro Murine lysyl oxida	AAB12307	. 21	641	12.0	591	19
	AAB00073	21	753	12.2	596	18
	AAB00077	21	774	12.2	2000	17
	AAB49534	2 7	57.7	13.5	043	15
Amino acid sequenc Human PRO229 prote	AAY13369	30	347	13.1	643	14
	AAW68200	13	347	13.1	643	13
Human liver cell c	AAW64537	19	347	13.1	545	13

ALIGNMENTS

RESULT

/SIDS8/gogdata/geneseq/geneseqp/AA1989.DAT:*/SIDS8/gogdata/geneseq/geneseqp/AA1990.DAT:*

/SIDS8/gcgdata/geneseq/genesedp/AA1991. /SIDS8/gcgdata/geneseq/geneseqp/AA1992

DAT: *

DAT: *

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Human; neurotrypsin; tumour inhibition; neurological disease; lung disease; gene therapy; drug development; stroke; brain injury; neurodegeneration; neuroinflammatory disease; multiple sclerosis; epilepsy; hypoxia; ischaemia; nerve transection; neoanglogenesis; emphysema; bronchitis.
      AAW83361 standard; Protein; 875 AA.
                                                                                                                                                                                                                          98WO-IB00625.
                                                                                                                                                                                                                                               97CH-0000966.
                                                  17-FEB-1999 (first entry)
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                                                                                                                                                                                                                                                                                                              WPI; 1999-009438/01.
                                                                                                                                                                                                                                                                    (SOND/) SONDEREGGER
                                                                        Human neurotrypsin.
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV72589
                                                                                                                                                                                                                                                                                          Sonderegger P;
                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                 W09849322-A1.
                                                                                                                                                                                                                          24-APR-1998;
                                                                                                                                                                                                                                               26-APR-1997;
                                                                                                                                                                                                      05-NOV-1998
                             AAW83361;
AAW83361
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New human and murine neurotrypsin - used, e.g. for inhibiting

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653
                                                                                                                                                                                                                                                                                            GRAYSRTLQQAAIPLLPKRFCCEERYKGRFTGRMLCAGNLHEHKRVDSCQGDSGGPLMCER 833
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                                                                                                                                                                                 HGDGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRVGDYHTLVPEEFEEEIGVQQIV 713
                                                                                                                                                                                                                                                                                                                     IHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLPLWRERPQKTASNCYITGWGDT 773
                                                                                                           ELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNE 353
                                                                       elyhagqwgtvcddqwddadaevicrqlglsgiakawhqayfgegsgpvmldevrctgne 300
LSIEQCPKSSWGEHNCGHKEDAGVSCTPLTDGVIRLAGGKGSHEGRLEVYYRGQWGTVCD 413
                                                                                                                                                                                                                                                         DGWTELNTYVVCRQLGFKYGKQASANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRH
                                                                                                                                                                        DCSHREDVSIACYPGGEGHRLSLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKD
                                                                                                                                                                                                           AAVICRQLGYKGPARARTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSE
                                                                                                                                                                                                                                                DAGVICDYFGKKASGNSNKESLSSVCGLRLLHRRQKRIIGGKNSLRGGWPWQVSLRLKSS
                            WSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVICSFSHGPTFPIIRLAGGSSVHEGRV
                                                                                                                                                                                                                                                                                                                                                                                              PGESWVVYGVTSWGYGCGVKDSPGVYTKVSAFVPWIKSVTKL 875
                                                                                                                                                                                                                                                                                                                                                                                                        Tsuruoka N, Yamaguchi N, Yamashiro K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW99088 standard; Protein; 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse serine protease BSSP-3
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                                                                                                            The present sequence is a serine protease designated BSSP-3, which is isolated from mouse brain tissue. Transformants may be used to produce the enzyme or its partial sequences. Products from the present invention are used for screening for potential peptide or non-peptide serine protease inhibitors or expression regulators for use as drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540
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                                                                                                                                                                                                                                                                                                                                               61 PLPRFPRPPRALPAQRPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLRWAEVPPFLE 120
                                                                                                                                                                                                                                                                                                                                                                         55 --prfplplripaaqrpqvlstghtpptiprrcgageswgnatnlgvpclhwdevppfle 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 GTVEVYASGVWGTVCSSHWDDSDASVICHQLQLGGKGIAKQTPFSGLGLIPIYWSNVRCR
                                               - used in screening
                                                                                                                                                                                                                                                                  Indels 114;
                                                                                                                                                                                                                                        Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New serine protease expressed in brain tissue - used been potential serine protease inhibitors for drug use
                                                                                                                                                                                                                                       71.0%; Score 3481; DB 20; 71.8%; Pred. No. 9.9e-242;
                                                                                                                                                                                                                                                                   47; Mismatches
                                                                                        Example 1; Page 51-54; 69pp; Japanese.
                                                                                                                                                                                                                                                      Best Local Similarity 71.89
Matches 628; Conservative
           1999-142942/12
                                                                                                                                                                                                     761 AA;
                         N-PSDB; AAX19027
                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 YHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNELS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356 IEQCPKSSWGEHNCGHKEDAGVSC-----TPLTDG-------VIRLAGGK 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           542 sapgnarfgggsgpivlddvrcsghe----sypwscphngwlshncghsedagvic 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               594 sasqsrptpspdtw---ptshastagsesslalrlvnggdrcqgrvevlyrgswgtvcdd 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 HWDDSDASVICHQLQLGGKGIAKQTPFS---GLGLIPIYWSNVRCRGDEENILLCEKDIW 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IIRLAGGSSVHEGRVEL 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 VPP----FLERSPPASWAQLRGQRHNFCRSPDGAGRPW-------CFYGDARGKV- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 ------DMGYCDCRHGS-----VRLRGGKNEFEGTVEVYASGVWGTVCSS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  434 gyesylwscphngwlshncqhsedag----vicsaahswstpspdtlptitlpastvgs 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 Q------RPHALQAGHTPRPHPWGCPAGEPWVSVTDFGAPCLR----WAE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GFDSVL-----NDSLHHSHRHSPPAGPHYPYYLPTQQRPPTTRPPPPLPRFPRPRALPA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.18; Score 983.5; DB 19; Length 1785; 28.88; Pred. No. 4.7e-62; Live 92; Mismatches 353; Indels 283;
                                                                                                                                                                                                                                                                                                                                                                         Proteins containing scavenger receptor, cysteine rich domain useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                              (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 QGGVCPQKMAAAVTCSFSHGPTFP----
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Fig 2; 54pp; German.
                                                                                                                                               98WO-DE00096
                                                                                                                                                                                      97DE-1030997
                                                                                                                                                                                                          97DE-1000519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 28.89
Matches 294; Conservative
                                                                                                                                                                                                                                                                                                                          WPI: 1998-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1785 AA;
                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV49652.
autoantibody; ss.
                                                                                                                                                                                                                                                                                        Mollenhauer J,
                                     Homo sapiens
                                                                                                                                                                                          8-JUL-1997;
                                                                                                                                                                                                          09-JAN-1997;
                                                                                                                                                   09-JAN-1998;
                                                                         WO9830687-A2
                                                                                                               16-JUL-1998
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Gene therapy; TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzahemer's disease; sanile dementia; Huntington's disease; amyotrophic lateral sclerosis; Parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychlatric; psychoactive substance use; anxiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1311 ay------fgsgsgpitlddvecsgtestlwqcrnrg--w-----fshncnhreda 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : | | : | 1.16 ptttttarp---sancggflfy----asglfsspsypayypnnakcvwelevnsgyri 1176
                                                                                                                                                                                                                                              1177 nlgfsnlkieahhncsfdyveifdgslnsslllgkic------ndtrq--ift 1221
                                                                                                                                      753 LWRERPQKTASNCYITG-WGDTGRAYSRTLQQAAIPLLPKRFCEERYKGRFTGRMLCAGN 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  812 LHEHKRVDSCQGDSGGPL-------MCERPGESWVYGVTSWGYGCGVKDSP 856
                                                                                                                                                                                                                                                                                                                       554 YFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC------DYFG 603
                                                                                                                                                                                                                                                                                                                                                                                                                                  604 KKASGNSNKESLSSVCGLRLHRRQKRIIGG------KNSLRGGWPWQV----- 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647 -----SLRLKSSHG------DGRLLCGATLLSSCWVLTAAHCFKRYGNSTRSYAVRV 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  693 GDYHTLVPEEFEEEIGVQQIVIHREYRPDRSDYDIALVRLQGPEEQCARFSSHVLPACLP 752
                                                                                                                                                                                                               494 LSLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARARTWA 553
                                                  888 drcrgrvevlyggswgtvcddywdtndanvvcrqlgcgwamsapgnaqfgggsgpivldd 947
394 GSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGKQASAN-HFEESTGPIWLDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McCarthy SA, Fraser CC, Sharp JD, Barnes TM;
                                                                                                             453 VSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB66088 standard; Protein; 1436 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAY-2000; 2000WO-US14858.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001
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TANGO protein; INTERCEPT protein; neurological disorder; central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzheiner's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep; neuropsychiatric; psychoactive substance use; anxiety.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TANGO and INTERCEPT nucleic acids, proteins, and antibodies, useful for screening assays and diagnostic assays and for the treatment of neurological diseases such as Alzheimer's, Parkinson's and Huntington's
                                                                                                                                                             1089 edagvicseft--alrlysetetescagrlevfyngtwgsvgrrnittaiagivcrqlgc 1146
                                                                                                                                                                                                                                                                                                                                                                                                                             -----rirvrggdtecsgrveiwhagswgtvcddswdlaeaevvcqqlgcgsalaa 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1309 slkslnassghlalilssifgllllvlfilfltwcrvqkqkhl------plrvst 1357
1147 gengvvslaplsktgsgfmwvddigcpkthisiwgclsapwerrisspaeetwitced-- 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 RTMAYFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGN 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---SLSSVCGLRLL-------HRRQKRIIGGKNSLRGGWPWQVSL 648
                                                                                                  EDAGVSCTPLTDGVIRLAGGKGSHE--GRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGF
                                                                                                                                                                                                                                -KYGKQASANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGG
                                                                                                                                                                                                                                                                                                                                                                     490 EGHRESLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66037 standard; Protein; 1453 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-032313/04
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                                                                                                            373
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central nervous system; focal brain disorder; bipolar affective disorder; global-diffuse cerebral disorder; cerebrovascular; Alzhelmer's disease; senile dementia; Huntington's disease; amyotrophic lateral sclerosis; parkinson's; Gilles de la Tourette's syndrome; hypertension; sleep;
                                                                                                                                                                                                                                                                                12;
central nervous system (CNS) disorders, CNS-related disorders, focal brain disorders, global-diffuse cerebral disorders and other meurological and cerebrovascular disorders. The CNS disorders include Alzheimer's disease, senile dementia, Huntington's disease, amyotrophic lateral sclerosis, Parkinson's, Gilles de la Tourette's syndrome, autronnafic function disorders such as hypertension and sleep disorders, neuropsychiatric disorders, psychoactive substance use disorders, and bipolar affective disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     956 gers----vrvwghrfhclgneslldncqmtvlgappcihgntvsvictgsltqplf 1008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDA 312
                                                                                                                                                                                                                                                                                                                     166 RHGSVRLRGGKNEFEGTVEVYASGVWGTVCSSHWDDSDASVICHQLQ-----LGGKGI 218
                                                                                                                                                                                                                                                                                                                                                        896 rytdvrlvngksqcdgqveinvlghwgslcdthwdpedarvlcrqlscgtalsttggkyi 955
                                                                                                                                                                                                                                                                                                                                                                                               219 AKQTPFSGLGLIPIYWSNVRCRGDEENILLCEKDIWQGGVCPQKMAAAVTCSFS-HGPTF 277
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373 EDAGVSCTPLTDGVIRLAGGKGSHE--GRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             490 EGHRLSLGFPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 DAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550 RIMAYFGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVICDYFGKKASGN
                                                                                                                                                                                                                                       16.8%; Score 822.5; DB 22; Length 1453; 34.7%; Pred. No. 1.3e-50; Live 73; Mismatches 188; Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; INTERCEPT protein; neurological disorder;
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                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 pI-----
                                                                                                                                                                                       1453 AA;
                                                                                                                                                                                                                                                                 Best Local Similarity
Matches 189; Conserv
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(GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                    486 ----YP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the ducts of von Ebner's gland and secreted into fluid bathing the taste buds contained in the taste papillae. It was identified by isolation of a rat cDNA (AAT44068) encoding a novel secreted protein of 1590 amino acids. The unique structure and localisation of regulation of taste sensation. Ebnerin suggest that it is a binding protein in saliva for regulation of taste sensation. Ebnerin can be used to develop prods, for investigating taste perception and to raise antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      313 DAEVICRQLGLSGIAKAWHQAYFGEGSGPVMLDEVRCTGNELSIEQCPKSSWGEHNCGHK 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -FSHGPTFP-----IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 VCSSHWDDSDASVICHQLQLGGKGIAKQTPFS---GLGLIPIYWSNVRCRGDEENILLCE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 hrgwlshncghqedagvicsdsqtssptpgwwnpggtnndviydtqettetsqtssptpd 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 mcddswdindanvvcrql---gcgwalsapgsaqfgqglgpivlddvacrgheaylwscs 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Von Ebner's gland derived polypeptide, ebnerin - useful to develop
prods. for investigating taste perception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%; Score 690.5; DB 18; Length 1290; dlarity 23.1%; Pred. No. 3.4e-41; Conservative 46; Mismatches 167; Indels 417;
                                                                                                                                                                                                                                           /label= Glycosylation
/note= "potential N-glycosylation site"
       /note= "potential N-glycosylation site"
950
                                                                                                                'note= "potential N-glycosylation site"
                                                                                                                                                  note- "potential N-glycosylation site"
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                                                                                                                                                                          label Glycosylation
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                                                                                                       'label = Glycosylation
                                                                                                                                       label- Glycosylation
                                   'label= Glycosylation
                                                                   /label= Glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 22-27; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in diagnostic assays.
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N-PSDB; AAT44068.
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Matches 189; Conserv.
                                                                                                                                1018
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                                                                                                                                                                 Modified-site
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Lymph node stromal cell; fsn -/- mice; inflammatory disorder; immune system disorder; cancer; viral disorder; HIV infection; blood vessel growth; tumour necrosis factor disorder; arthritis; inflammatory bowel disease; fibroblast growth factor-mediated disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           717 rlvngtnrcegrveilyrgswvpcaddswdindanvvcrqlgcgsalsapgnawfgggsg 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 dgsngsftstqnfmsvvfitdgsvtrrgfqadyystpirtsttppttfpiltgndsslvl 716
                                                                                                                                                                                                                                                                                                                                                                                                            417 wttkysssvpttgfptiadwwttpspeytcgglltlpyggfsspyypgsypnnarclwki 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 fvssmnrvtvvftdvqleggcnydyilvfdgpennssliarvcdgfngsftstqnfmsvv 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    537 fitdgsvtrrgfqadyystpiststtspttfpivtdwwttpspeytcgglltlpygqfss 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                597 pyypgsypnnarclwkifvpsmnrvtvvftdvqleggcnydyilgfdgpeynssllarvc 656
                                                                                                                                                                                                                                                                    238 edagvicsysqtssptpdsqtssptpgwwnpggtnndvsygpeqttdatdsglavrlvng 297
                                                                                                                 393 KGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQL--GFKYGKQASANHFEESTGPIWL 450
                                                                                                                                                298 gdrcqgrveilyggswgtycddswdtkdanvvcrqlvcgwalsapgsa-hfgqgsgsgsivl 356
-----TPLTDG--VIRLAGG 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide isolated from lymph node stromal cells of fsn -/- mice.
                                                                                                                                                                                                                                           451 DDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIAC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          561 PIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 599
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This is the amino acid sequence of a novel protein (see AAW68200), termed SP alpha, that is a member of the scavenger receptor cysteine-rich (SRCR) family. The sequence was deduced from an isolated cDNA clone (see AAV54605). SP alpha transcripts are found in human bone marrow, spleen, lymph node, thymus and foetal liver organisation as the extracellular region of CD5 and CD6 and is composed of 3 SRCR domains. It is capable of binding to cells of the monocytic lineage, and appears to be involved in the regulation of monocytic lineage, and appears to be involved in the regulation of monocyte activation, function and/or survival, and is therefore an important component in the immunoregulatory system. Methods of recombinantly producing SP alpha are disclosed. In addition, and interaction between SPalpha and its receptor. Sp alpha can be used in pharmaceutical compositions to regulate the immune response in, for example, autoimmune disease, viral infections, transplant rejection suppression, tumour cell proliferation suppression, and combined variable immunodeficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New scavanger receptor cysteine-rich protein - the antibodies of
                                                                                                                                                                                                                                     SP alpha; scavenger receptor; SRCR; human; antibody; immunoassay; immunomodulator; autoimmune disease; transplant rejection; infection; tumour; immunodeficiency; therapy.
                301 ygpgygriwldnvrcsgeeqsleqcqhrfwgfhdcthqedvavic 345
555 FGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           which can be used to modulate the immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "cysteine-rich domain"
138..239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "cysteine-rich domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "cysteine-rich domain"
                                                                                                                                                                                                          Human scavenger receptor protein SP alpha.
                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                       /label= Mat_protein
                                                                                                                AAW68200 standard; Protein; 347 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Siadak AW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0039956.
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                                                                                                                                                                               07-DEC-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9839443-A1
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                                                                                                                                               AAW68200;
                                                                                                                                                                                                                                                                                                                                                       Peptide
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                                                                                    280 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 339
                                                                                                                                   340 G------PVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC-----TP 381
                                                                                                                                                  382 LTDGVIRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGK----QAS 437
                                                                                                                                                                                                                                 438 ANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLG 497
                                                                                                                                                                                                                                                                                498 FPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARA---RTMAY 554
                                                              48; Gaps
                                                                                                     Length 347;
                                                               Indels
                                                                                                                                                                                                                                                                                                                                555 FGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 599
                                                                                                                                                                                                                                                                                                                                             301 ygpgygriwldnvrcsgeeqsleqcqhrfwgfhdcthqedvavic 345
                                                                45; Mismatches 114;
                                        13.1%; Score 643; DB 19; 40.0%; Pred. No. 1.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of protein PRO229.
                                                                                                                                                                                                                                                                                                                                                                                                                      AAY13369 standard; Protein; 347 AA
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97US-0059115.
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97US-0059263
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97US-0062285
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                                                                Matches 138; Conservative
                                                      Local Similarity
        347 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9914328-A2
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17-SEP-1997
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          Seguence
                                         Query Match
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transmembrane PRO polypeptides. The PRO polypeptides are useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma), gastrointestinal disorders (e.g. enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease), wound repair, cardiovascular disorders (e.g. parkinson's disease), wound repair, cardiovascular disorders (e.g. roheamia, atherosclerosis), inflammatory disorders (e.g. aathma diabetes and retinal disorders such as retinitis and disorders such retinal disorders such as retinitis pigmentosum. The PRO nucleic acids have applications in molecular biology, including use as hybridization probes, and in chromosome and gene mapping.
                                                                                                                                                                 Sixty one nucleic acids encoding PRO polypeptides which are useful in the treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous cell carcinoma) and neurodegenerative diseases (e.g.
    Goddard A;
Fong S, Gao W, Gerber H, Gerritsen ME, Goddaré
Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
an J, Paoni NF, Roy MA, Stewart TA, Tumas D;
                                                                                                                                                                                                                                                                                                                   The present sequence is one of sixty one novel secreted and
                                                                                                                                                                                                                                                                              Claim 1; Fig 54; 393pp; English
                                                  an J, Pac
Wood WI;
                                                                                                                                                                                                                                    Alzheimer's disease)
                                                                                                          WPI; 2001-081051/09.
                                             Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 AA;
                                                                                                                                N-PSDB; AAF72398
      Filvaroff E,
                                                                   Williams PM,
                          Godowski PJ,
                                               Mather JP,
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438 ANHFEESTGPIWLDDVSCSGKETRFLQCSRRQWGRHDCSHREDVSIACYPGGEGHRLSLG 497 280 IRLAGGSSVHEGRVELYHAGQWGTVCDDQWDDADAEVICRQLGLSGIAKAWHQAYFGEGS 339 340 G------PVMLDEVRCTGNELSIEQCPKSSWGEHNCGHKEDAGVSC-----TP 381 382 LTDGVIRLAGGKGSHEGRLEVYYRGQWGTVCDDGWTELNTYVVCRQLGFKYGK----QAS 437 -----p 241 Query Match 13.1%; Score 643; DB 22; Length 347; Best Local Similarity 40.0%; Pred. No. 1.8e-38; Matches 138; Conservative 45; Mismatches 114; Indels 48; Gaps FPVRLMDGENKKEGRVEVFINGQWGTICDDGWTDKDAAVICRQLGYKGPARA---RTMAY 554 191 cnkhaygrkpiwlsqmscsgreatlqdcpsgpwgkntcnhdedtwveced---FGEGKGPIHVDNVKCTGNERSLADCIKQDIGRHNCRHSEDAGVIC 599 555 δ g ŏ Q Óλ QQ g õ g δ

Sequence

301

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